

**AMENDMENTS TO THE CLAIMS:**

Please replace the claims with the claims provided in the listing below wherein status, amendments, additions and cancellations are indicated.

1. (Previously Presented) Method for recording sequence information on biological compounds, comprising the steps of:

dividing one of text data representing a sequence of said biological compounds and numerical data obtained by converting said text data, utilizing a conversion rule, into a plurality of m-bit partial data arranged in a plurality of columns in an arranged direction corresponding to a direction along which said biological compounds are placed and in a plurality of rows in a non-arranged direction which crosses said arranged direction, where m is an integer greater than or equal to 16;

computing a first set of parity information by applying a first operation of a Galois field  $GF(2^m)$  along said non-arranged direction to a set of said partial data of each column;

computing a second set of parity information by applying a second operation of a Galois field  $GF(2^m)$  along said arranged direction to a set of said partial data of each row; and

representing said sequence information on said biological compounds by said first and second sets of parity information.

2. (Previously Presented) Method of claim 1, wherein  
when  $\alpha$  is a primitive element of a Galois field GF( $2^m$ ),  
said first set of parity information includes a sum of a plurality of products obtained  
by multiplying a set of said partial data of each column along said non-arranged  
direction by  $\alpha^{sp}$ ,  $\alpha^{s(p+1)}$ ,  $\alpha^{s(p+2)}$ , ...,  $\alpha^{s(p+dp)}$ , where s and p are nonnegative integers and  
dp is an integer greater than or equal to one; and

said second set of parity information includes a sum of a plurality of products  
obtained by multiplying a set of said partial data of each row along said arranged  
direction by  $\alpha^{tq}$ ,  $\alpha^{t(q+1)}$ ,  $\alpha^{t(q+2)}$ , ...,  $\alpha^{t(q+dq)}$ , where t and q are nonnegative integers and  
dq is an integer greater than or equal to one.

3. (Currently amended) Method of claim 2, wherein  
a number of said partial data placed along said arranged direction is  
smaller fewer than a number of said partial data placed along said non-arranged  
direction; and  
a number of data in said second set of parity information is smaller fewer  
than a number of data in said first set of parity information.

4. (Previously Presented) Method of claim 3, wherein said number of  
said partial data placed along said non-arranged direction is less than or equal to

$(2^m - 1)/4$ .

5. (Previously Presented) Method of claim 2, wherein both of said integers s and t are zero.

6. (Previously Presented) Method of claim 2, wherein both of said integers s and t are one.

7. (Previously Presented) Method of claim 2, wherein said first set of parity information includes a plurality of said sums obtained for each column using mutually different values of said integer s; and said second set of parity information includes a plurality of said sums obtained for each row using mutually different values of said integer t.

8. (Previously Presented) Method of claim 1, wherein said partial data is said numerical data obtained by expressing each of said biological compounds as data having a size less than or equal to six bits.

9. (Previously Presented) Method of claim 1, wherein said integer m that defines said Galois field  $GF(2^m)$  is a multiple of 64.

10. (Currently amended) Method of claim 1, further comprising the steps of:

making an assumption that said sequence of said biological compounds is a standard first sequence and another sequence of biological compounds is a second sequence;

computing two sets of parity information on [[a]] said second sequence of biological compounds subject to examination, said two sets of parity information on said second sequence of biological compounds subject to examination corresponding to said two sets of parity information on said standard first sequence; and

identifying differences between said standard first sequence and said second sequence of biological compounds subject to examination, by using said two sets of parity information on said standard first sequence and said two sets of parity information on said second sequence of biological compounds subject to examination.

11. (Previously Presented) Method of claim 1, wherein said biological compounds are nucleotides constituting at least part of DNA, RNA, or a gene.

12. (Previously Presented) Method of claim 1, wherein said biological compounds are amino acids constituting at least part of a protein.

13. (Previously Presented) Device for recording sequence information on biological compounds, comprising:

a sequencer for reading sequence information on said biological compounds;

dividing means for dividing one of text data representing a sequence of said biological compounds and numerical data obtained by converting said text data utilizing a conversion rule, into a plurality of m-bit partial data arranged in a plurality of columns in an arranged direction corresponding to a direction along which said biological compounds are placed, and in a plurality of rows in a non-arranged direction which crosses said arranged direction, where m is an integer greater than or equal to 16;

computing means for computing a first set of parity information by applying a first operation of a Galois field  $GF(2^m)$  along said non-arranged direction to a set of said partial data of each column and computing a second set of parity information by applying a second operation of a Galois field  $GF(2^m)$  along said arranged direction to a set of said partial data of each row; and

recording means for recording said first and second sets of parity information in a recording medium.

14. (Previously Presented) Device of claim 13, wherein

when  $\alpha$  is a primitive element of a Galois field  $GF(2^m)$ ,

said first set of parity information includes a sum of a plurality of products obtained by multiplying a set of said partial data of each column along said non-arranged direction by  $\alpha^{sp}$ ,  $\alpha^{s(p+1)}$ ,  $\alpha^{s(p+2)}$ , ...,  $\alpha^{s(p+dp)}$ , where s and p are nonnegative integers and dp is an integer greater than or equal to one; and

said second set of parity information includes a sum of a plurality of products obtained by multiplying a set of said partial data of each row along said arranged direction by  $\alpha^{tq}$ ,  $\alpha^{t(q+1)}$ ,  $\alpha^{t(q+2)}$ , ...,  $\alpha^{t(q+dq)}$ , where t and q are nonnegative integers and dq is an integer greater than or equal to one.

15. (Previously Presented) Computer-readable medium for storing sequence information on biological compounds, comprising:

a data structure stored in said medium, wherein,  
one of text data representing a sequence of said biological compounds and numerical data obtained by converting said text data utilizing a conversion rule is divided into a plurality of m-bit partial data arranged in a plurality of columns in an arranged direction, corresponding to a direction along which said biological compounds are placed, and in a plurality of rows in a non-arranged direction which crosses said arranged direction, where m is an integer greater than or equal to 16;

a first set of parity information is computed by applying a first operation of a Galois field GF(2<sup>m</sup>) along said non-arranged direction to a set of said partial data

of each column and a second set of parity information is computed by applying a second operation of a Galois field GF( $2^m$ ) along said arranged direction to a set of said partial data of each row; and

    said first and second sets of parity information are recorded in said data structure as said sequence information on said biological compounds.

16. (Previously Presented) Computer-readable medium of claim 15,  
wherein

    said data structure further includes a mathematical digest of one of said text data representing said sequence of said biological compounds and said numerical data corresponding to said text data, and

    said mathematical digest has a size greater than or equal to 40 bits.

17. (Previously Presented) Method for supplying sequence information on biological compounds, comprising the steps of:

    recording one of text data representing a sequence of said biological compounds and numerical data obtained by converting said text data utilizing a conversion rule, in a first file;

    dividing said one of text data and numerical data recorded in said first file into a plurality of m-bit partial data arranged in a plurality of columns in an arranged direction corresponding to a direction along which said biological

compounds are placed, and in a plurality of rows in a non-arranged direction which crosses said arranged direction, where m is an integer greater than or equal to 16;

computing a first set of parity information by applying a first operation of a Galois field GF( $2^m$ ) along said non-arranged direction to a set of said partial data of each column, and computing a second set of parity information by applying a second operation of a Galois field GF( $2^m$ ) along said arranged direction to a set of said partial data of each row;

recording said first and second sets of parity information in a second file; and

providing said two sets of parity information recorded in said second file through a communications network.

18. (Previously Presented) Method for utilizing sequence information on biological compounds, comprising the steps of:

receiving through said communications network from a supplier said two sets of parity information recorded on said second file, according to claims 17;

identifying differences between said sequence of said biological compounds held by said supplier and a sequence of biological compounds subject to examination, based on said two sets of received parity information; and

when said differences cannot be recovered, receiving sequence

information on a part corresponding to said differences, within said one of text data and numerical data recorded in said first file, through said communications network from said supplier.

19. (Previously Presented) Method of claim 18, wherein when  $\alpha$  is a primitive element of a Galois field GF( $2^m$ ), said first set of parity information includes a sum of a plurality of products obtained by multiplying a set of said partial data of each column along said non-arranged direction by  $\alpha^{sp}$ ,  $\alpha^{s(p+1)}$ ,  $\alpha^{s(p+2)}$ , ...,  $\alpha^{s(p+dp)}$ , where s and p are nonnegative integers and dp is an integer greater than or equal to one; and said second set of parity information includes a sum of a plurality of products obtained by multiplying a set of said partial data of each row along said arranged direction by  $\alpha^{tq}$ ,  $\alpha^{t(q+1)}$ ,  $\alpha^{t(q+2)}$ , ...,  $\alpha^{t(q+dq)}$ , where t and q are nonnegative integers and dq is an integer greater than or equal to one.

20. (Previously Presented) Method of claim 17, further comprising the step of:  
providing information on a number of said sequence of said biological compounds, and information on a mathematical digest of said one of text data and numerical data through said communications network.

21. (Previously Presented) Method for recording sequence information on biological compounds, comprising the steps of:

dividing one of text data representing a sequence of said biological compounds and numerical data obtained by converting said text data utilizing a conversion rule, into a plurality of m-bit partial data arranged in a plurality of columns in an arranged direction corresponding to a direction along which said biological compounds are placed, and in a plurality of rows in a non-arranged direction which crosses said arranged direction, where m is an integer greater than or equal to 16;

making assumptions that a maximum value of said partial data is Nmax, and a prime number larger than said maximum value Nmax is P;

computing a first set of parity information by applying a first operation of a Galois field GF(P) along said non-arranged direction to a set of said partial data of each column;

computing a second set of parity information by applying a second operation of a Galois field GF(P) along said arranged direction to a set of said partial data of each row; and

representing said sequence information on said biological compounds by said first and second sets of parity information.

22. (Previously Presented) Method of claim 21, wherein

said maximum value Nmax of said partial data is smaller than ( $2^m - 1$ ) and said prime number P satisfies the following condition:

$$2^m > P > N_{\text{max}}$$

23. (Previously Presented) Method of claim 22, wherein  
when  $\delta$  is a primitive element of a Galois field GF(P),  
said first set of parity information includes a sum of a plurality of products obtained by multiplying a set of said partial data of each column along said non-arranged direction by  $\delta^{sp}$ ,  $\delta^{s(p+1)}$ ,  $\delta^{s(p+2)}$ , ...,  $\delta^{s(p+dp)}$ , where s and p are nonnegative integers and dp is an integer greater than or equal to one; and

said second set of parity information includes a sum of a plurality of products obtained by multiplying a set of said partial data of each row along said arranged direction by  $\delta^{tq}$ ,  $\delta^{t(q+1)}$ ,  $\delta^{t(q+2)}$ , ...,  $\delta^{t(q+dq)}$ , where t and q are nonnegative integers and dq is an integer greater than or equal to one.

24. (Previously Presented) Method for supplying sequence information on biological compounds, comprising the steps of:

recording one of text data representing the sequence of said biological compounds and numerical data obtained by converting said text data utilizing a conversion rule, in a first file;

dividing said one of said text data and said numerical data recorded in said

first file into a plurality of m-bit partial data arranged in a plurality of columns in an arranged direction corresponding to a direction along which said biological compounds are placed, and in a plurality of rows in a non-arranged direction which crosses said arranged direction, where m is an integer larger than or equal to 16;

making assumptions that a maximum value of said partial data is Nmax, and a prime number larger than said maximum value Nmax is P;

computing a first set of parity information by applying a first operation of a Galois field GF(P) along said non-arranged direction to a set of said partial data of each column and computing a second set of parity information by applying a second operation of a Galois field GF(P) along said arranged direction to a set of said partial data of each row;

recording said first and second sets of parity information in a second file; and

providing said two sets of parity information recorded in said second file through a communications network.

25. (Previously Presented) Method for utilizing sequence information on biological compounds comprising the steps of:

receiving through said communications network from a supplier said two sets of parity information recorded in said second file, according to claim 24;

identifying differences between said sequence of said biological compounds held by said supplier and a sequence of biological compounds subject to examination, based on said two sets of received parity information; and when said differences cannot be recovered, receiving sequence information on a part corresponding to said differences, within said one of text data recorded in said first file, through said communications network from said supplier.

26. (Previously Presented) Method of claim 18, further comprising the step of:

accessing at least one of information on a number of said sequence of said biological compounds, and information on a mathematical digest of said one of text data and numerical data, through said communications network.